RAW SEQUENCE LISTING
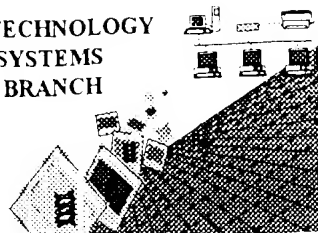# ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

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TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/661,992A_

Source: _1600_

Date Processed by STIC: _11/21/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio** (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
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3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 01/29/2002

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/661,992 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
     Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
     Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
     "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
     (OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
     (NEW RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
     (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>
     Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
     "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING

DATE: [illegible]

PATENT APPLICATION: US/09/661,992A

TIME: [illegible]

Input File : A:\237 sequence listing.asc

Output File: N:\CRF4\11212002\I661992A.raw

```
 3  <110> APPLICANT: Scheirlinger, Friedrich
 4        Herschbauner, Randolf
 5        Falkner, Falke-Guenter
 6        Dorner, Friedrich
```

W--> 8 <120> *← mandatory number identified and response needed*

W--> 10 <130> FILE REFERENCE:

```
12 <140> CURRENT APPLICATION NUMBER: US 09/661,992A     ← again the mandatory number identified
```

C--> 14 <141> CURRENT FILING DATE: 2000-09-14 *← child of this and response*

```
14 <160> NUMBER OF SEQ ID NOS: 106
16 <170> SOFTWARE: PatentIn Ver. 2.1
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Does Not Comply
Correction Also Needed

1-13

ERRORED SEQUENCES

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18 <210> SEQ ID NO: 1
19 <211> LENGTH: 26
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of the artificial sequence:primer
26 <400> SEQUENCE: 1
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E--> 27 ctcaattttc ttgtccacct tggtgc *← 26 (global error) violation 1 (?)*

Error summary sheet

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28 26
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 26
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Description of the artificial sequence:primer
39 <400> SEQUENCE: 2
```

E--> 40 ctcgattctc ttgatcaact cagtct *same error*

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41 26
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 24
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
51 <223> OTHER INFORMATION: Description of the artificial sequence:primer
52 <400> SEQUENCE: 3
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E--> 53 tggaatgggc acatgcagat ctct *same*

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54 24
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 24
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RAW SEQUENCE LISTING

DATE: 11 ...

PATENT APPLICATION: US/09/661,992A

TIME: 1:...

Input Set : A:\237 sequence listing.asc
Output Set : N:\CRF4\11212002\I661992A.raw

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      <211> TYPE: DNA
      <213> ORGANISM: Artificial Sequence
      <220> FEATURE:
      <223> OTHER INFORMATION: Description of the artificial sequence:primer
      <400> SEQUENCE: 4
E--> 66 ctcattcctg ttgaagctct tgac
      24
  763 <210> SEQ ID NO: 50
  764 <211> LENGTH: 57
  765 <212> TYPE: DNA
  766 <213> ORGANISM: Artificial Sequence
  768 <220> FEATURE:
  769 <223> OTHER INFORMATION: Description of the artificial sequence:primer
  771 <400> SEQUENCE: 50
E--> 772 catgccatga ctcgcggccc agccggccat ggccsaggts marctgcags agtcwgg
  773 57
  776 <210> SEQ ID NO: 51
  777 <211> LENGTH: 56
  778 <212> TYPE: DNA
  779 <213> ORGANISM: Artificial Sequence
  781 <220> FEATURE:
  782 <223> OTHER INFORMATION: Description of the artificial sequence:primer
  784 <400> SEQUENCE: 51
E--> 785 gtcctcgcaa ctgcggccca gccggccatg gccgaggtgc agcttcagga gtcagg
  788 56
  789 <210> SEQ ID NO: 52
  790 <211> LENGTH: 56
  791 <212> TYPE: DNA
  792 <213> ORGANISM: Artificial Sequence
  794 <220> FEATURE:
  795 <223> OTHER INFORMATION: Description of the artificial sequence:primer
  797 <400> SEQUENCE: 52
E--> 798 gtcctcgcaa ctgcggccca gccggccatg gccgatgtgc agcttcagga gtcrgg
  749 56
  802 <210> SEQ ID NO: 53
  803 <211> LENGTH: 56
  804 <212> TYPE: DNA
  805 <213> ORGANISM: Artificial Sequence
  807 <220> FEATURE:
  808 <223> OTHER INFORMATION: Description of the artificial sequence:primer
  810 <400> SEQUENCE: 53
E--> 811 gtcctcgcaa ctgcggccca gccggccatg gcccaggtgc agctgaagsa gtcagg
  812 56
  815 <210> SEQ ID NO: 54
  816 <211> LENGTH: 56
  817 <212> TYPE: DNA
  818 <213> ORGANISM: Artificial Sequence
  820 <220> FEATURE:
  821 <223> OTHER INFORMATION: Description of the artificial sequence:primer
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<210> <400> SEQUENCE: 14

E--> 824 gtcctcgcaa ctgcggccca gccggccatg gccgaggtyc agctgcarca rtctgg

<210> SEQ ID NO: 55
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence:primer
<400> SEQUENCE: 55

E--> 837 gtcctcgcaa ctgcggccca gccggccatg gcccaggtyc arctgcagca gyctgg

841 <210> SEQ ID NO: 56
842 <211> LENGTH: 56
843 <212> TYPE: DNA
844 <213> ORGANISM: Artificial Sequence
846 <220> FEATURE:
847 <223> OTHER INFORMATION: Description of the artificial sequence:primer
849 <400> SEQUENCE: 56

E--> 850 gtcctcgcaa ctgcggccca gccggccatg gccgargtga agctggtgga rtctgg

851 56
854 <210> SEQ ID NO: 57
855 <211> LENGTH: 56
856 <212> TYPE: DNA
857 <213> ORGANISM: Artificial Sequence
859 <220> FEATURE:
860 <223> OTHER INFORMATION: Description of the artificial sequence:primer
862 <400> SEQUENCE: 57

E--> 863 gtcctcgcaa ctgcggccca gccggccatg gccgaggttc agcttcagca gtctgg

864 56
867 <210> SEQ ID NO: 58
868 <211> LENGTH: 56
869 <212> TYPE: DNA
870 <213> ORGANISM: Artificial Sequence
872 <220> FEATURE:
873 <223> OTHER INFORMATION: Description of the artificial sequence:primer
875 <400> SEQUENCE: 58

E--> 876 gtcctcgcaa ctgcggccca gccggccatg gccgaagtgc agctgktgga gwctgg

877 56
880 <210> SEQ ID NO: 59
881 <211> LENGTH: 56
882 <212> TYPE: DNA
883 <213> ORGANISM: Artificial Sequence
885 <220> FEATURE:
886 <223> OTHER INFORMATION: Description of the artificial sequence:primer
888 <400> SEQUENCE: 59

E--> 889 gtcctcgcaa ctgcggccca gccggccatg gcccagatcc agttgctgca gtctgg

890 56
893 <210> SEQ ID NO: 60

RAW SEQUENCE LISTING

```
894 <211> LENGTH: 60
895 <212> TYPE: DNA
896 <213> ORGANISM: Artificial Sequence
898 <220> FEATURE:
899 <223> OTHER INFORMATION: Description of the artificial sequence:primer
901 <400> SEQUENCE: 60
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E--> 902 accgccagag gcgcgcccac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc
```
903 60
```
E--> 904 ttggcccc
```
905 68
908 <210> SEQ ID NO: 61
909 <211> LENGTH: 68
910 <212> TYPE: DNA
911 <213> ORGANISM: Artificial Sequence
913 <220> FEATURE:
914 <223> OTHER INFORMATION: Description of the artificial sequence:primer
916 <400> SEQUENCE: 61
```
E--> 917 accgccagag gcgcgcccac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc
```
918 60
921 <210> SEQ ID NO: 62
922 <211> LENGTH: 60
923 <212> TYPE: DNA
924 <213> ORGANISM: Artificial Sequence
926 <220> FEATURE:
927 <223> OTHER INFORMATION: Description of the artificial sequence:primer
929 <400> SEQUENCE: 62
```
E--> 930 accgccagag gcgcgcccac ctgaaccgcc tccacctgag gagactgtga gagtggtgcc
```
931 60
934 <210> SEQ ID NO: 63
935 <211> LENGTH: 60
936 <212> TYPE: DNA
937 <213> ORGANISM: Artificial Sequence
939 <220> FEATURE:
940 <223> OTHER INFORMATION: Description of the artificial sequence:primer
942 <400> SEQUENCE: 63
```
E--> 943 accgccagag gcgcgcccac ctgaaccgcc tccacctgca gagacagtga ccagagtccc
```
944 60
947 <210> SEQ ID NO: 64
948 <211> LENGTH: 60
949 <212> TYPE: DNA
950 <213> ORGANISM: Artificial Sequence
952 <220> FEATURE:
953 <223> OTHER INFORMATION: Description of the artificial sequence:primer
955 <400> SEQUENCE: 64
```
E--> 956 accgccagag gcgcgcccac ctgaaccgcc tccacctgag gagacggtga ctgaggttcc
```
957 60
960 <210> SEQ ID NO: 65
961 <211> LENGTH: 60
962 <212> TYPE: DNA
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/661,992A

DATE: 11 21 02
TIME: 1 46 16

Input Set : A:\237 sequence listing.asc
Output Set : N:\CRF4\11212002\I661992A.raw

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence:mychis (
<400> SEQUENCE: 67

E--> 969 ggttcagatg ggcgcgcctc tggcggtggc ggatcggaca ttgagctcac ccagtctcca

1142 <210> SEQ ID NO: 79
1143 <211> LENGTH: 74
1144 <212> TYPE: DNA
1145 <213> ORGANISM: Artificial Sequence
1147 <220> FEATURE:
1148 <223> OTHER INFORMATION: Description of the artificial sequence:mychis (
1150 <400> SEQUENCE: 79

E--> 1151 ggccgcagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca
1152 60

E--> 1153 ccatcactaa taag
1154 74
1157 <210> SEQ ID NO: 80
1158 <211> LENGTH: 74
1159 <212> TYPE: DNA
1160 <213> ORGANISM: Artificial Sequence
1162 <220> FEATURE:
1163 <223> OTHER INFORMATION: Description of the artificial sequence:mychis
1165 <400> SEQUENCE: 80

E--> 1166 aattcttatt agtgatggtg atggtgatgt gccgccccat tcagatcctc ttctgagatg
1167 60

E--> 1168 agttttttgtt ctgc
1169 74
1172 <210> SEQ ID NO: 81
1173 <211> LENGTH: 726
1174 <212> TYPE: DNA
1175 <213> ORGANISM: Artificial Sequence
1177 <220> FEATURE:
1178 <223> OTHER INFORMATION: Description of the artificial sequence:scFv region
1180 <400> SEQUENCE: 81

E--> 1181 gaggtgaagc tggtggagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc
1182 60

E--> 1183 tcctgcaagg cttctgggta tatcttcaca aactatggaa tgaactgggt gaagcaggct
1184 120

E--> 1185 ccaggaaagg gtttaaagtg gatgggctgg ataaacacct acactggaga gccaacatat
1186 180

E--> 1187 gctgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccag cactgcctat
1188 240

E--> 1189 ttgcagatca acaacctcaa aaatgaggac acggctacat atttctgtgc attatatggt
1190 300

E--> 1191 aactcccta aggggtttgc ttactggggc caagggactc tggtcactgt ctctgcaggt
1192 360

E--> 1193 ggaggcggtt caggtgggcg cgcctctggc ggtggcggat cggatattca gatgacacag
1194 420

RAW SEQUENCE LISTING

PATENT APPLICATION N: US/09/661,992A

Input Set : A:\237 sequence listing.asc
Output Dir: N:\CRF4\11212002\I661992A.raw

E--> 1195 tctcccaaat tcctgcttgt atcagcagga gacagggtta ccataacctg caaggccagt
```
1196 480
```
E--> 1197 cagagtgtga gtaatgatgt agcttggtac caacagaagc cggggcagtc tcctaaacta
```
1198 540
```
E--> 1199 ctgatgtact atgcatccaa tcgctacact ggagtccctg atcgcttcac tggcagtgga
```
1200 600
```
E--> 1201 tatgggacgg atttcacttt caccatcagc actgtgcagg ctgaagacct ggcagtttat
```
1202 660
```
E--> 1203 ttctgtcagc aggattatgg ctctcctccc acgttcggag ggggcaccaa gctggaaatt
```
1204 720
```
E--> 1205 aaacgg
```
1206 726
1267 <210> SEQ ID NO: 83
1268 <211> LENGTH: 747
1269 <212> TYPE: DNA
1270 <213> ORGANISM: Artificial Sequence
1272 <220> FEATURE:
1273 <223> OTHER INFORMATION: Description of the artificial sequence:scFv region
1275 <400> SEQUENCE: 83
```
E--> 1276 gaagtgcagc tggtggagtc tggggggaggc ctagtgaagc ctggagggtc cctgaaactc
```
1277 60
```
E--> 1278 tcctgtgcag cctctggatt cactttcagt acctatacca tgtcttgggt tcgccagact
```
1279 120
```
E--> 1280 ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagtta cacctactat
```
1281 180
```
E--> 1282 ccagacagtg tgaggggccg attcaccatc tccagagaca atgccaagaa caccctgtac
```
1283 240
```
E--> 1284 ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtac aagagatggg
```
1285 300
```
E--> 1286 ggacacgggt acggtagtag ctttgactac tggggccaag gcaccactct cacagtctcc
```
1287 360
```
E--> 1288 tcaggtggag gcggttcagg tgggcgcgcc tctggcggtg gcggatcgca aattgtgctc
```
1289 420
```
E--> 1290 acccagtctc cactctccct gcctgtcagt cttggagatc aagcctccat ctcttgcaga
```
1291 480
```
E--> 1292 tctagtcaga gcattgtaca tagtaatgga aacacctatt tagaatggta cctgcagaaa
```
1293 540
```
E--> 1294 ccaggccagt ctccaaagct cctgatctac aaagtttcca accgattttc tggggtccca
```
1295 600
```
E--> 1296 gacaaattca gtggcagtgg atcagggaca gatttcacac tcaagatcag cagagtggag
```
1297 660
```
E--> 1298 gctgaggatc tgggagttta ttactgcttt caaggttcac atgttccgtg gacgttcggt
```
1299 720
```
E--> 1300 ggaggcacca agctggaaat caaacgg
```
1301 747
1457 <210> SEQ ID NO: 97
1458 <211> LENGTH: 747
1459 <212> TYPE: DNA
1460 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/661,992A

Input Set : A:\237 sequence listing.asc
Output Set : N:\CRF4\11212002\I661992A.raw

1461 <220> FEATURE:
1463 <223> OTHER INFORMATION: Description of the artificial sequence:scFv region
1465 <400> SEQUENCE: 87

E--> 1466 gaggtgcagc ttcaggagtc aggggggaggc ttagtgaagc ctggagggtc cctgaaactc

1467 60

E--> 1468 tcctgtgcag cctctggatt cattttttagt agttatacca tgtcttgggt tcgccagact

1469 120

E--> 1470 ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagttc cacctactat

1471 180

E--> 1472 ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac

1473 240

E--> 1474 ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcactgtac aagagagggg

1475 300

E--> 1476 ggtggttatt acgtcaactg gtacttcgat gtctggggcg caggcaccac tctcacagtc

1477 360

E--> 1478 tcctcaggtg gaggcggttc aggtgggcgc gcctctggcg gtggcggatc ggacattgag

1479 420

E--> 1480 ctcacncagt ctccagcttc tttggctgtg tctctagggc agagggccac catatcctgc

1481 480

E--> 1482 agagccagtg aaagtgttga tagttatggc aagagtttta tgcactggta ccagcagaaa

1483 540

E--> 1484 ccagggcagc cacccaaact cctcatctat cgtgcatcca acctagaatc tgggatccct

1485 600

E--> 1486 gccaggttca gtggcagtgg gtctaggaca gacttcaccc tcaccattaa tcctgtggag

1487 660

E--> 1488 gctgatgatg ttgcnaccta ttactgtcag caaagtaatg aggatcccct cacgttcggt

1489 720

E--> 1490 gctgggacca gactggaaat aaaacgg

1491 747

1552 <210> SEQ ID NO: 89
1553 <211> LENGTH: 2199
1554 <212> TYPE: DNA
1555 <213> ORGANISM: Artificial Sequence
1557 <220> FEATURE:
1558 <223> OTHER INFORMATION: Description of the artificial sequence:scFv region
1560 <400> SEQUENCE: 89

E--> 1561 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc

1562 60

E--> 1563 atggcggagg tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggtccctg

1564 120

E--> 1565 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc

1566 180

E--> 1567 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc

1568 240

E--> 1569 tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc

1570 300

E--> 1571 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga

1572 360

E--> 1573 gagggggggtg gtttcaccgt caactggtac ttcgatgtct ggggcgcagg aacctcagtc

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/661,992A

DATE: 11.21...
TIME: 1:1...

Input Set : A:\237 sequence listing.asc
Output Set: N:\CRF4\11212002\I661992A.raw

```
E--> 1575 accgtctcct caggtggagg cggttcaggt gggcgcgcct ctggcggtgg cggatcggac
E--> 1577 attgtgctga cacagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccata
E--> 1579 tcctgcagag ccagtgaaag tgttgatagt tatggctata attttatgca ctggtatcag
E--> 1581 cagataccag gacagccacc caaactcctc atctatcgtg catccaacct agagtctggg
E--> 1583 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct
E--> 1585 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg
E--> 1587 ttcggtactg ggaccagact ggaaataaaa cgggcggccg cagcccgggc accagaaatg
E--> 1589 cctgttctgg aaaaccgggc tgctcagggc gatattactg cacccggcgg tgctcgccgt
E--> 1591 ttaacgggtg atcagactgc cgctctgcgt gattctctta gcgataaacc tgcaaaaaat
E--> 1593 attattttgc tgattggcga tgggatgggg gactcggaaa ttactgccgc acgtaattat
1594 1020
E--> 1595 gccgaaggtg cgggcggctt ttttaaaggt atagatgcct taccgcttac cgggcaatac
1596 1080
E--> 1597 actcactatg cgctgaataa aaaaaccggc aaaccggact acgtcaccga ctcggctgca
1598 1140
E--> 1599 tcagcaaccg cctggtcaac cggtgtcaaa acctataacg gcgcgctggg cgtcgatatt
1600 1200
E--> 1601 cacgaaaaag atcacccaac gattctggaa atggcaaaag ccgcaggtct ggcgaccggt
1602 1260
E--> 1603 aacgtttcta ccgcagagtt gcaggatgcc acgcccgctg cgctggtggc acatgtgacc
1604 1320
E--> 1605 tcgcgcaaat gctacggtcc gagcgcgacc agtgaaaaat gtccgggtaa cgctctggaa
1606 1380
E--> 1607 aaaggcggaa aaggatcgat taccgaacag ctgcttaacg ctcgtgccga cgttacgctt
1608 1440
E--> 1609 ggcggcggcg caaaaaacctt tgctgaaacg gcaaccgctg gtgaatggca gggaaaaacg
1610 1500
E--> 1611 ctgcgtgaac aggcacaggc gcgtggttat cagttggtga gcgatgctgc ctcactgaat
1612 1560
E--> 1613 tcggtgacgg aagcgaatca gcaaaaaccc ctgcttggcc tgtttgctga cggcaatatg
1614 1620
E--> 1615 ccagtgcgct ggctaggacc gaaagcaacg taccatggca atatcgataa gcccgcagtc
1616 1680
E--> 1617 acctgtacgc caaatccgca acgtaatgac agtgtaccaa ccctggcgca gatgaccgac
1618 1740
E--> 1619 aaagccattg aattgttgag taaaaatgag aaaggctttt tcctgcaagt tgaaggtgcg
1620 1800
E--> 1621 tcaatcgata aacaggatca tgctgcgaat ccttgtgggc aaattggcga gacggtcgat
1622 1860
```

file://C:\CRF4\Outhold\VsrI661992A.htm

11/21/02

RAW SEQUENCE LISTING

E--> 1623 ctcgatgaag ccgtacaacg ggcgctggaa ttcgctaaaa aggagggtaa cacgctggtc
1624 1200

E--> 1625 atagtcaccg ctgatcacgc ccacgccagc cagattgttg cgccggatac caaagctccg
1626 1260

E--> 1627 ggcctcaccc aggcgctaaa taccaaagat ggcgcagtga tggtgatgag ttacgggaac
1617 1640

E--> 1629 tccgaagagg attcacaaga acataccggc agtcagttgc gtattgcggc gtatggcccg
1630 2175

E--> 1631 catgccgcca atgttgttgg actgaccgac cagaccgatc tcttctacac catgaaagcc
1632 2160

E--> 1633 gctctggggg atatcgcaca ccatcaccat caccattaa
1634 2199
1785 <210> SEQ ID NO: 91
1786 <211> LENGTH: 909
1787 <212> TYPE: DNA
1788 <213> ORGANISM: Artificial Sequence
1790 <220> FEATURE:
1791 <223> OTHER INFORMATION: Description of the artificial sequence:scFv region
1793 <400> SEQUENCE: 91

E--> 1794 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc
1795 60

E--> 1796 atggcggagg tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggtccctg
1797 120

E--> 1798 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc
1799 180

E--> 1800 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc
1801 240

E--> 1802 tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc
1803 300

E--> 1804 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga
1805 360

E--> 1806 gagggggtg gtttcaccgt caactggtac ttcgatgtct ggggcgcagg aacctcagtc
1807 420

E--> 1808 accgtctcct caggtggagg cggttcaggt gggcgcgcct ctggcggtgg cggatcggac
1809 480

E--> 1810 attgtgctga cacagtntcc agcttctttg gctgtgtctc tagggcagag ggccaccata
1811 540

E--> 1812 tcntgcagag ccagtgaaag tgttgatagt tatggctata attttatgca ctggtatcag
1813 600

E--> 1814 cagataccag gacagccacc caaactcctc atctatcgtg catccaacct agagtctggg
1815 660

E--> 1816 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct
1817 720

E--> 1818 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg
1819 780

E--> 1820 ttcggtactg ggaccagact ggaaataaaa cgggcggccg caccgaagcc ttccactccg
1821 840

E--> 1822 cccgggtctt cccgtatgaa acagctggaa gacaaagtag aggagctcct tagcaagaac
1823 900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/661,992A

DATE: ...
TIME: ...

Input Set : A:\237 sequence listing.asc
Output Set: N:\CRF4\11212002\I661992A.raw

E--> 1824 taccatctag aaaacgaggt agctcgtctg aaaaagcttg ttggtgaacg tggtggtcac
     ...

E--> 1826 catcaccatc accattaa
     ...
     <210> SEQ ID NO: 99
     <211> LENGTH: ...
     <212> TYPE: DNA
     <213> ORGANISM: Artificial Sequence
     <220> FEATURE:
     <223> OTHER INFORMATION: Description of the artificial sequence:scFv region
     <400> SEQUENCE: 99

E--> 2306 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc
     2307 60

E--> 2308 atggccgagg tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggtccctg
     2309 120

E--> 2310 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc
     2311 180

E--> 2312 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc
     2313 240

E--> 2314 tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc
     2315 300

E--> 2316 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga
     2317 360

E--> 2318 gaggggggtg gtttcaccgt caactggtac ttcgatgtct ggggcgcagg aacctcagtc
     2319 420

E--> 2320 accgtctcct caggtggagg cggttcaggt gggcgcgcct ctggcggtgg cggatcggac
     2321 480

E--> 2322 attgtgctga cacagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccata
     2323 540

E--> 2324 tcctgcagag ccagtgaaag tgttgatagt tatggctata attttatgca ctggtatcag
     2325 600

E--> 2326 cagataccag gacagccacc caaactcctc atctatcgtg catccaacct agagtctggg
     2327 660

E--> 2328 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct
     2329 720

E--> 2330 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg
     2331 780

E--> 2332 ttcggtactg ggaccagact ggaaataaaa cgggcggccg cagaacaaaa actcatctca
     2333 840

E--> 2334 gaagaggatc tgaatggggc ggcacatcac catcaccatc actaataa
     2335 888

<210> 87
<211> 747
<212> DNA
<213> Artificial
Sequence

<220>
<223> Description of the artificial sequence:scFv
region

<400> 87
gaggtgcagc ttcaggagtc aggggggaggc ttagtgaagc
ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt catttttagt agttatacca
tgtcttgggt tcgccagact 120
ccggagaaga ggctggagtg ggtcgcaacc attagtagtg
gtggtagttc cacctactat 180
ccagacagtg tgaagggccg attcaccatc tccagagaca
atgccaagaa cacectgtac 240
ctgcaaatga gcagtctgaa gtctgaggac acagccatgt
atcactgtac aagagagggg 300
ggtggttatt acgtcaactg gtacttcgat gtctggggcg
caggcaccac tctcacagtc 360
tcctcaggtg gaggcggttc aggtgggcgc gcctctggcg
gtggcggatc ggacattgag 420
ctcacncagt ctccagcttc tttggctgtg tctctagggc
agagggccac catatcctgc 480
agagccagtg aaagtgttga tagttatggc aagagtttta
tgcactggta ccagcagaaa 540
ccagggcagc cacccaaact cctcatctat cgtgcatcca
acctagaatc tggatccct 600
gccaggttca gtggcagtgg gtctaggaca gacttcaccc
tcaccattaa tcctgtggag 660
gctgatgatg ttgcnaccta ttactgtcag caaagtaatg
aggatcccct cacgttcggt 720

<210> 88
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:scFv
region

<400> 88
Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys
Pro Gly Gly
 1   5   10
 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe
          Ser Ser Tyr 20   25
          30

all amino acid sequence show the linea described in Item 1.05 Error summary sheet

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/09/661,992A

INPUT DOC : A:\237 sequence listing.asc

OUTPUT FILE: N:\CRF4\11212002\I661992A.raw

User Explanation

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:47; N Pos. 4??,???
Seq#:79; N Pos. 22?
Seq#:91; N Pos. 22?,4??,???
Seq#:92; Xaa Pos. 10?
Seq#:99; N Pos. 21?
Seq#:105; Xaa Pos. 2,5,14,15

← These required
show the above that

PATENT APPLICATION: US/09/661,992A   DATE: 11-21-...
                                             TIME: 1 ...:..

Input Set : A:\237 sequence listing.asc
Output Set: N:\CRF4\11212002\I661992A.raw

L:... M:110 W: Mandatory field data missing, FIELD TITLE INVENTION
L:... M:001 W: Mandatory field data missing, FIELD FILE REFERENCE
L:... M:170 E: Current Filing Date differs, Replaced Current Filing Date
L:... M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:1
L:... M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:2
L:... M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:3
L:... M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:4
L:772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:50
L:781 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:51
L:798 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:52
L:811 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:53
L:824 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:54
L:837 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:55
L:850 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:56
L:863 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:57
L:876 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:58
L:889 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:56 SEQ:59
L:902 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:60
M:254 Repeated in SeqNo=60
L:917 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:61
L:930 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:62
L:943 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:63
L:956 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:64
L:969 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:65
L:982 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:66
L:995 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:67
L:1008 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:68
L:1021 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:69
L:1034 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:70
L:1047 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:71
L:1060 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:72
L:1073 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:59 SEQ:73
L:1086 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:74
L:1099 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:75
L:1112 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:76
L:1125 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:77
L:1138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:78
L:1151 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:79
M:254 Repeated in SeqNo=79
L:1166 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:80
M:254 Repeated in SeqNo=80
L:1181 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:81
M:254 Repeated in SeqNo=81
L:1276 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:83
M:254 Repeated in SeqNo=83
L:1371 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:85
M:254 Repeated in SeqNo=85
L:1466 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:87

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/661,992A

DATE: ░░░░░

TIME: ░░░░░

Input Set : A:\237 sequence listing.asc
Output Set: N:\CRF4\11212002\I661992A.raw

M:254 Repeated in SeqNo=87
L:1437 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:87
L:1464 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:87
L:1464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:42
L:1477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:89
L:1541 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:87 SEQ:87
M:254 Repeated in SeqNo=89
L:1567 M:254 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:89
L:1567 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:89
L:1567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:127
L:1794 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:87 SEQ:91
M:254 Repeated in SeqNo=91
L:1800 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:91
L:1800 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:91
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:16?
L:1810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:4?
L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:54?
L:1869 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:92
L:1869 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:92
L:1869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:92 after pos.:140
L:2312 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:99
L:2312 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:99
L:2312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:180
L:2552 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:105
L:2552 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:105
L:2552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105 after pos.:0